

PCT10

RAW SEQUENCE LISTING DATE: 04/11/2002 PATENT APPLICATION: US/10/089,019 TIME: 16:07:33

Input Set : A:\USSEQLIST.TXT

Output Set: N:\CRF3\04112002\J089019.raw

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4 <110> APPLICANT: DEWOLF, WALTER E. JR
      5
              KALLENDER, HOWARD
              LONSDALE, JOHN T.
      8 <120> TITLE OF INVENTION: METHODS FOR MAKING AND USING FATTY ACID
              SYNTHESIS PATHWAY REAGENTS
     12 <130> FILE REFERENCE: GM50068
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/089,019
     15 <141> CURRENT FILING DATE: 2002-03-25
     17 <150> PRIOR APPLICATION NUMBER: PCT/US00/29451
     18 <151> PRIOR FILING DATE: 2000-10-26
     20 <150> PRIOR APPLICATION NUMBER: 60/161,775
     21 <151> PRIOR FILING DATE: 1999-10-27
     23 <160> NUMBER OF SEQ ID NOS: 37
     25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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     28 <211> LENGTH: 999
     29 <212> TYPE: DNA
     30 <213> ORGANISM: Staphylococcus aureus
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     35 ggtatggcac aagatttgtt taataacaat gatcaagcaa ctgaaatttt aacttcagca 180
     36 gcaaagacgt tagactttga tattttagag acaatgttta ctgatgaaga aggtaaattg 240
     37 ggtgaaactg aaaacacgca accagcttta ttgacgcata gttcggcatt attagcagcg 300
     38 ctaaaaattt tgaatcctga ttttactatg gggcatagtt taggtgaata ttcaagttta 360
     39 gttgcagctg acgtattatc atttgaagat gcagttaaaa ttgttagaaa acgtggtcaa 420
    40 ttaatggcgc aagcatttcc tactggtgta ggaagcatgg ctgcagtatt gggattagat 480
    41 tttgataaag tcgatgaaat ttgtaagtca ttatcatctg atgacaaaat aattgaacca 540
    42 gcaaacatta attgcccagg tcaaattgtt gtttcaggtc acaaagcttt aattgatgag 600
    43 ctagtagaaa aaggtaaatc attaggtgca aaacgtgtca tgcctttagc agtatctgga 660
    44 ccattccatt catcgctaat gaaagtgatt gaagaagatt tttcaagtta cattaatcaa 720
    45 tttgaatggc gtgatgctaa gtttcctgta gttcaaaatg taaatgcgca aggtgaaact 780
    46 gacaaagaag taattaaatc taatatggtc aagcaattat attcaccagt acaattcatt 840
    47 aactcaacag aatggctaat agaccaaggt gttgatcatt ttattgaaat tggtcctgga 900
    48 aaagttttat ctggcttaat taaaaaaata aatagagatg ttaagttaac atcaattcaa 960
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    52 <211> LENGTH: 332
    53 <212> TYPE: PRT
    54 <213> ORGANISM: Staphylococcus aureus
    56 <400> SEQUENCE: 2
    57 Met Gly His His His His His His His His His Ser Ser Gly His
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59 Ile Glu Gly Arg His Met Leu Glu Met Ser Lys Thr Ala Ile Ile Phe
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61 Pro Gly Gln Gly Ala Gln Lys Val Gly Met Ala Gln Asp Leu Phe Asn
63 Asn Asn Asp Gln Ala Thr Glu Ile Leu Thr Ser Ala Ala Lys Thr Leu
64
                            55
65 Asp Phe Asp Ile Leu Glu Thr Met Phe Thr Asp Glu Glu Gly Lys Leu
66 65
                        70
                                             75
                                                                  80
67 Gly Glu Thr Glu Asn Thr Gln Pro Ala Leu Leu Thr His Ser Ser Ala
68
                    85
                                         90
69 Leu Leu Ala Ala Leu Lys Ile Leu Asn Pro Asp Phe Thr Met Gly His
                100
                                    105
                                                         110
71 Ser Leu Gly Glu Tyr Ser Ser Leu Val Ala Ala Asp Val Leu Ser Phe
72
            115
                                120
73 Glu Asp Ala Val Lys Ile Val Arg Lys Arg Gly Gln Leu Met Ala Gln
74
       130
                                                 140
75 Ala Phe Pro Thr Gly Val Gly Ser Met Ala Ala Val Leu Gly Leu Asp
76 145
                        150
                                             155
                                                                 160
77 Phe Asp Lys Val Asp Glu Ile Cys Lys Ser Leu Ser Ser Asp Asp Lys
78
                    165
                                         170
79 Ile Ile Glu Pro Ala Asn Ile Asn Cys Pro Gly Gln Ile Val Val Ser
80
                180
                                    185
                                                         190
81 Gly His Lys Ala Leu Ile Asp Glu Leu Val Glu Lys Gly Lys Ser Leu
82
           195
                                200
                                                     205
83 Gly Ala Lys Arg Val Met Pro Leu Ala Val Ser Gly Pro Phe His Ser
84
       210
                            215
                                                 220
85 Ser Leu Met Lys Val Ile Glu Glu Asp Phe Ser Ser Tyr Ile Asn Gln
86 225
                        230
                                             235
87 Phe Glu Trp Arg Asp Ala Lys Phe Pro Val Val Gln Asn Val Asn Ala
88
                    245
                                        250
89 Gln Gly Glu Thr Asp Lys Glu Val Ile Lys Ser Asn Met Val Lys Gln
90
               260
                                    265
                                                         270
91 Leu Tyr Ser Pro Val Gln Phe Ile Asn Ser Thr Glu Trp Leu Ile Asp
92
           275
                                280
                                                     285
93 Gln Gly Val Asp His Phe Ile Glu Ile Gly Pro Gly Lys Val Leu Ser
94
       290
                            295
                                                 300
95 Gly Leu Ile Lys Lys Ile Asn Arg Asp Val Lys Leu Thr Ser Ile Gln
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                                                                 320
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103 <212> TYPE: PRT
104 <213> ORGANISM: Staphylococcus aureus
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110
                20
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111 Ala Thr Glu Ile Leu Thr Ser Ala Ala Lys Thr Leu Asp Phe Asp Ile
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113 Leu Glu Thr Met Phe Thr Asp Glu Glu Gly Lys Leu Gly Glu Thr Glu
114
         50
                             55
                                                  60
115 Asn Thr Gln Pro Ala Leu Leu Thr His Ser Ser Ala Leu Leu Ala Ala
116 65
                         70
                                              75
117 Leu Lys Ile Leu Asn Pro Asp Phe Thr Met Gly His Ser Leu Gly Glu
118
                     85
                                                              95
119 Tyr Ser Ser Leu Val Ala Ala Asp Val Leu Ser Phe Glu Asp Ala Val
120
                 100
                                     105
                                                          110
121 Lys Ile Val Arg Lys Arg Gly Gln Leu Met Ala Gln Ala Phe Pro Thr
122
            115
                                 120
                                                      125
123 Gly Val Gly Ser Met Ala Ala Val Leu Gly Leu Asp Phe Asp Lys Val
124
        130
                             135
                                                  140
125 Asp Glu Ile Cys Lys Ser Leu Ser Ser Asp Asp Lys Ile Ile Glu Pro
126 145
                         150
                                              155
                                                                  160
127 Ala Asn Ile Asn Cys Pro Gly Gln Ile Val Val Ser Gly His Lys Ala
128
                     165
                                         170
                                                              175
129 Leu Ile Asp Glu Leu Val Glu Lys Gly Lys Ser Leu Gly Ala Lys Arg
130
                180
                                     185
131 Val Met Pro Leu Ala Val Ser Gly Pro Phe His Ser Ser Leu Met Lys
132
            195
                                 200
                                                      205
133 Val Ile Glu Glu Asp Phe Ser Ser Tyr Ile Asn Gln Phe Glu Trp Arg
134
        210
                             215
                                                  220
135 Asp Ala Lys Phe Pro Val Val Gln Asn Val Asn Ala Gln Gly Glu Thr
136 225
                         230
                                             235
                                                                  240
137 Asp Lys Glu Val Ile Lys Ser Asn Met Val Lys Gln Leu Tyr Ser Pro
138
                    245
                                         250
139 Val Gln Phe Ile Asn Ser Thr Glu Trp Leu Ile Asp Gln Gly Val Asp
140
                260
                                     265
                                                          270
141 His Phe Ile Glu Ile Gly Pro Gly Lys Val Leu Ser Gly Leu Ile Lys
142
            275
                                 280
                                                      285
143 Lys Ile Asn Arg Asp Val Lys Leu Thr Ser Ile Gln Thr Leu Glu Asp
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146 305
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150 <211> LENGTH: 1001
151 <212> TYPE: DNA
152 <213> ORGANISM: Staphylococcus aureus
154 <400> SEQUENCE: 4
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157 tattttgagc aatttttaga tacatctgat gaatggattt ctaagatgac tggaattaaa 180
158 gaaagacatt gggcagatga cgatcaagat acttcagatt tagcatatga agcaagtgta 240
159 aaagcaatcg ctgacgctgg tattcagcct gaagatatag atatgataat tgttgccaca 300
160 gcaactggag atatgccatt tccaactgtc gcaaatatgt tgcaagaacg tttagggacg 360
161 ggcaaagttg cctctatgga tcaacttgca gcatgttctg gatttatgta ttcaatgatt 420
162 acagctaaac aatatgttca atctggagat tatcataata ttttagttgt cggtgcagat 480
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		ggttctgatg gcactggtgg taaacattta tatttagata aagatactgg taaactgaaa 6																	
166	atg	atgaatggtc gagaagtatt taaatttgct gttagaatta tgggtgatgc atcaacacgt 72 gtagttgaaa aagcgaattt aacatcagat gatatagatt tatttattcc tcatcaagct 78														720			
167	gta	gttg	aaa	aagc	gaat	tt a	acat	caga	t ga	tata	gatt	tat	780						
168	8 aatattagaa ttatggaatc agctagagaa cgcttaggta													tttcaaaaga caaaatgagt					
	gtttctgtaa ataaatatgg aaatacttca gctgcgtcaa																		
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						at g	acaa	taaa	a tg	ggga	aaat	a					1001		
				D NO															
				H: 3															
				PRT															
						phyl	ococ	cus	aure	us									
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185	Ser	Asp	Glu	Trp	Ile	Ser	Lys	Met	Thr	Gly	Ile	Lys	Glu	Arq	His	Trp			
186		50					55			-		_		_					
187	Ala	Asp	Asp	Asp	Gln	Asp	Thr	Ser	Asp	Leu	Ala	Tyr	Glu	Ala	Ser	Val			
188		_	_	_		70			•		75	•				80			
189	Lys	Ala	Ile	Ala	Asp	Ala	Gly	Ile	Gln	Pro	Glu	Asp	Ile	Asp	Met				
190	•				85		1			90					95				
191	Ile	Val	Ala	Thr		Thr	Glv	Asp	Met		Phe	Pro	Thr	Va l	Ala	Asn			
192				100			1		105					110	mu	11011			
	Met	Leu	Gln		Ara	Leu	Glv	Thr		Lvs	Val	Δla	Ser		Asp	G1n			
194			115		<b>5</b>		1	120	<b>4-1</b>	-15	, 42		125	1100	nop	OIII			
	Leu	Ala		Cvs	Ser	Glv	Phe		Tvr	Ser	Met	Tle		Δla	Lys	Gln			
196		130		-1-			135		-1-		1100	140	~ ***	mu	шуз	GIII			
	Tvr		Gln	Ser	Glv	Asp		His	Asn	Tle	Len		Va 1	Glv	Ala	Δen			
198		,	<b></b>	701		150	- <u>7</u> -	1110	11011	110	155	Val	val	GLY	ALU	160	Ci		
		Leu	Ser	Tivs	Tle		Asn	T.e.ii	Thr	Δcn		Sor	ጥስ <u>ዮ</u>	בות	Val				
200		204		LJD	165	* ***	nsp	Пец	1111	170	ALG	DET	TIIT	мта	175	Leu			
	Phe	Glv	Asn	Glv		Glv	λla	Val	T10		Cly	G1 <sub>11</sub>	Va I	C02	Glu	C1			
202	1 110	OL y	пор	180	AIU	Gry	AIG	Val	185	TTE	GIY	GIU	val		GIU	GTÀ			
	Δγα	Glv	Tla		Sar	Фил	Clu	Mot		Con	7 an	C1**	шhъ	190	<b>61</b>	T			
204	Arg	Gry	195	116	ser	тут	GIU		GTÀ	Ser	ASP	СТА		GIY	Gly	гĀг			
	Uic	T 011		Tou	λαν	T ***	N an	200	<i>α</i> 1	T	T	T	205	3	<b>a</b> 3	•			
206	птъ		тут	Leu	ASP	гЛЯ		THE	GIY	гла	Leu		met	Asn	Gly	Arg			
	<i>α</i> 3	210	Dha	T	nh -	21-	215	3	<b>-1</b> -	37 - 1	<b>a</b> 3	220		_	_,	_			
		Val	Pne	ьys	Pne		val	Arg	тте	met	_	Asp	Ala	Ser	Thr	_			
208		**- 7	<b>01</b>	_		230	_	_,			235	_ •			_	240			
	val	val	GIU	гла		Asn	ьeu	Thr	Ser		Asp	Ile	Asp	Leu	Phe	Ile			
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214			275					280					205			
		Ser			Sor	Tlo	Dro			Tla	7.00	Ø1 m	285		<b>-</b>	
216		290		AIG	DET	TTE	295		261	тте	ASP			ьeu	ьуs	Asn
				T.tre	λcn	λan			т1.	17a 1	Τ	300		Dl	<b>a</b> 1.	<b>~</b> 3
	305		шец	пуъ	ASP	310		TILL	тте	val			GTA	Pne	GLY	Gly
			mh~	m~~	C1			mh se	<b>T1</b>	<b>T</b>	315		_			320
220	GTA	пец	1111	тър	325	Ald	Met	THE	TTE		Trp	GTĀ	Lys			
	<b>~21</b>	ر ام	EO T	ח אור						330						
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					<b>Q</b> .1	Ctanharlagague										
						Staphylococcus aureus										
				NCE:		1			_	) _ <b>_</b>						
		ser	HIS	met		val	GLY	He	Lys		Phe	Gly	Ala	Tyr	Ala	Pro
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	GLu	Lys	He		Asp	Asn	Ala	Tyr		Glu	Gln	Phe	Leu	Asp	Thr	Ser
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244			115					120					125			
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252				180					185					190		
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259	Gln	Ala	Asn	Ile	Arg	Ile	Met	Glu	Ser	Ala	Arg	Glu	Arq	Leu	Glv	
260					245					250	J	- 3-	٠,		255	
261	Ser	Lys	Asp	Lys	Met	Ser	Val	Ser	Val		Lys	Tvr	Glv	Asn		Ser
262		_	•	260					265		_1 _	- <b>1</b> -	- <b>-</b> 1	270	<del></del>	~ ~ .
	Ala	Ala	Ser		Pro	Leu	Ser	Ile		Gln	Glu	Leu	Lvs		Glv	Tive
264			275		_			280	P		~		285		~-J	_, 5
	Leu	Lys		Asp	Asp	Thr	Ile		Len	Va 1	Gly	Phe		Glv	Glv	Τ.Δ.1
		•	-	_	- T.				~	. — —	1		1	-1	I	<b></b>

VERIFICATION SUMMARY

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L:14 M:270 C: Current Application Number differs, Replaced Current Application Number